RADemics

# Multi-Cancer Early Screening Frameworks Using AI and Genomic Data

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## Abstract

Cancer remains one of the leading causes of mortality worldwide due to late diagnosis, tumor heterogeneity, and limitations of conventional single-organ screening approaches. Multi-cancer early detection (MCED) frameworks have emerged as a transformative strategy in oncology by enabling simultaneous identification of multiple cancer types through minimally invasive blood-based diagnostics. Integration of artificial intelligence (AI) with genomic and multi-omics data has accelerated the development of advanced computational systems capable of analyzing circulating tumor DNA, cell-free DNA methylation patterns, transcriptomic alterations, and proteomic signatures for early cancer prediction and tissue-of-origin classification. Deep learning architectures, including transformer models and neural networks, facilitate extraction of complex nonlinear patterns from high-dimensional biological datasets, while explainable artificial intelligence enhances interpretability and clinical trust in predictive outcomes. Cloud computing and high-performance computing infrastructures further strengthen scalability, enabling real-time analysis of large-scale genomic datasets and supporting collaborative precision oncology research. Clinical applications of MCED systems extend to early diagnosis, risk stratification, treatment monitoring, and recurrence surveillance, offering significant potential to improve patient survival outcomes and reduce healthcare burden. The notable progress, challenges related to data heterogeneity, model generalization, ethical governance, regulatory validation, and clinical integration continue to restrict large-scale adoption. Continuous advancements in multimodal data fusion, federated learning, and precision medicine frameworks are expected to further enhance the accuracy, reliability, and clinical applicability of AI-driven MCED systems.

**Keywords:** Multi-cancer early detection, Artificial intelligence, Genomics, Liquid biopsy, Multi-omics integration, Precision oncology, Explainable AI, Deep learning, Cancer screening.

## Introduction

Cancer represents a leading global health challenge, driven by increasing incidence rates, late-stage diagnosis, and biological heterogeneity across tumor types [1]. Conventional screening approaches remain largely organ-specific, relying on imaging modalities, histopathological evaluation, and biochemical assays designed for individual cancers [2]. Such methods often fail to capture early molecular alterations that precede clinical manifestation, resulting in delayed detection and reduced therapeutic effectiveness [3]. Variability in tumor progression, absence of symptoms during initial stages, and limited population-wide screening coverage further contribute to poor survival outcomes across multiple cancer types [4]. The growing burden of cancer

necessitates a shift from isolated diagnostic strategies toward integrated, systemic screening frameworks capable of identifying malignancies at their earliest stages using minimally invasive approaches [5].

Multi-cancer early detection systems have emerged as a promising paradigm in precision oncology, enabling simultaneous screening of diverse malignancies through analysis of circulating molecular biomarkers [6]. Blood-based diagnostics involving circulating tumor DNA, cell-free DNA fragments, methylation signatures, and exosomal components provide critical insights into tumor biology without requiring invasive tissue sampling [7]. These molecular signals reflect early oncogenic transformations and capture tumor-derived alterations that circulate within the bloodstream [8]. The ability to detect multiple cancers from a single sample introduces a scalable and efficient screening strategy with potential to significantly reduce diagnostic delays and improve clinical outcomes [9]. Such systems represent a transition from traditional reactive oncology models toward proactive and preventive cancer care frameworks [10].

Advances in genomic technologies and multi-omics profiling have significantly expanded the scope of cancer biomarker discovery [11]. High-throughput sequencing techniques enable comprehensive characterization of genomic mutations, epigenetic modifications, transcriptomic dysregulation, and proteomic variations associated with tumor initiation and progression [12]. Integration of these heterogeneous biological datasets provides a multidimensional view of cancer development, revealing complex molecular interactions underlying disease evolution [13]. The high dimensionality and complexity of such datasets necessitate advanced computational methods capable of extracting meaningful patterns from large-scale biological information [14]. This requirement has positioned artificial intelligence as a central component in modern cancer diagnostics and biomarker interpretation [15].